

<!--StartFragment-->ALIGNMENTS

RESULT 1

Q4W8A9_9CAUL

ID Q4W8A9_9CAUL Unreviewed; 257 AA.
 AC Q4W8A9;
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2005, sequence version 1.
 DT 05-FEB-2008, entry version 11.
 DE Carotenoid C2-hydroxylase.
 GN Name=crtG;
 OS Brevundimonas sp. SD212.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Brevundimonas.
 OX NCBI_TaxID=281067;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SD212;
 RX PubMed=16085816; DOI=10.1128/AEM.71.8.4286-4296.2005;
 RA Nishida Y., Adachi K., Kasai H., Shizuri Y., Shindo K., Sawabe A.,
 RA Komemushi S., Miki W., Misawa N.;
 RT "Elucidation of a carotenoid biosynthesis gene cluster encoding a
 RT novel enzyme, 2,2'-beta-hydroxylase, from Brevundimonas sp. strain
 RT SD212 and combinatorial biosynthesis of new or rare xanthophylls.";
 RL Appl. Environ. Microbiol. 71:4286-4296(2005).
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 CC -----
 DR EMBL; AB181388; BAD99415.1; -; Genomic_DNA.
 DR GO; GO:0003824; F:catalytic activity; IEA:InterPro.
 DR GO; GO:0008152; P:metabolic process; IEA:InterPro.
 DR InterPro; IPR006088; Sterol_desatur.
 DR Pfam; PF01598; Sterol_desat; 1.
 PE 4: Predicted;
 SQ SEQUENCE 257 AA; 28641 MW; 35F465E7EC8A125C CRC64;

Query Match 100.0%; Score 1391; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 1.4e-109;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLRDL	LITTLALS	LIIGLRYLLVGAAAHG	LLWAGAGRGRALNLRPPAMKRIRAEIVASLI	60
Db	1	MLRDL	LITTLALS	LIIGLRYLLVGAAAHG	LLWAGAGRGRALNLRPPAMKRIRAEIVASLI	60
Qy	61	ACPIYALPAALVLELWKRGGTAIYSDPD	AWPLWWLPVSLIVYLLAHDAFY	YWVHRALHHP		120
Db	61	ACPIYALPAALVLELWKRGGTAIYSDPD	AWPLWWLPVSLIVYLLAHDAFY	YWVHRALHHP		120
Qy	121	RVFGWAHA	AEHHRSDPSAFASFAFDPAEAAATAWFLPALALIVPIHWGVALTLLT	LM	SLT	180
Db	121	RVFGWAHA	AEHHRSDPSAFASFAFDPAEAAATAWFLPALALIVPIHWGVALTLLT	LM	SLT	180
Qy	181	AALNHAGRE	VWPAAWLERAPLRWLI	TATHHDAH	HKRFNGNYGLYFQF	WDRWAGTEVSAAP 240
Db	181	AALNHAGRE	VWPAAWLERAPLRWLI	TATHHDAH	HKRFNGNYGLYFQF	WDRWAGTEVSAAP 240
Qy	241	SPPSPVIPPERPSAPLR				257
Db	241	SPPSPVIPPERPSAPLR				257

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RESULT 2
Q0GXS3_9CAUL
ID   Q0GXS3_9CAUL               Unreviewed;          257 AA.
AC   Q0GXS3;
DT   03-OCT-2006, integrated into UniProtKB/TrEMBL.
DT   03-OCT-2006, sequence version 1.
DT   05-FEB-2008, entry version 8.
DE   2,2'-beta-ionone ring hydroxylase.
GN   Name=crtG;
OS   Brevundimonas aurantiaca.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC   Caulobacteraceae; Brevundimonas.
OX   NCBI_TaxID=74316;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 15266;
RX   PubMed=16781830; DOI=10.1016/j.gene.2006.04.017;
RA   Tao L., Rouviere P.E., Cheng Q.;
RT   "A carotenoid synthesis gene cluster from a non-marine Brevundimonas
RT   that synthesizes hydroxylated astaxanthin.";
RL   Gene 379:101-108(2006).
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CC   -----
DR   EMBL; DQ497427; ABF50965.1; -; Genomic_DNA.
DR   GO; GO:0003824; F:catalytic activity; IEA:InterPro.
DR   GO; GO:0008152; P:metabolic process; IEA:InterPro.
DR   InterPro; IPR006088; Sterol_desatur.
DR   Pfam; PF01598; Sterol_desat; 1.
PE   4: Predicted;
SQ   SEQUENCE 257 AA; 28653 MW; 5FE010220DF75FE1 CRC64;

Query Match          98.4%; Score 1369; DB 2; Length 257;
Best Local Similarity 98.8%; Pred. No. 1.1e-107;
Matches 254; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MLRDLLITTALSLIIGLRYLLVGAAAHGLLWAGAGRGRALNLRPPAMKRIRAEIVASLI 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLRDLLITTALSLIIGLRYLLVGAAAHGLLWAGAGRGRALNLRPPAMKRIRAEIVASLI 60

Qy      61 ACPIYALPAALVLELWKRGGTAIYSDPDWPLWWLPVSLIVYLLAHDAFYVWVHRALHHP 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACPIYALPAALVLELWKRGGTAIYSDPDWPLWWLPVSLIVYLLAHDAFYVWVHRALHHP 120

Qy      121 RVFGWAHAEHHRSDPSAFASFAFDPAEAAAATAWFLPALALIVPIHWGVALTLLTLMslt 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 RVFGWAHAEHHRSDPSAFASFAFDPAEAAAATAWFLPALALIVPIHWGVALTLLTLMslt 180

Qy      181 AALNHAGREVWPAAWLERAPLRWLITATHHDAHKKRFNGNYGLYFQFWRWAGTEVSAAP 240
      ||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      181 AALNHAGSEVWPAAWLERAPLRWLITATHHDAHKKRFNGNYGLYFQFWRWAGTEVSAAP 240

Qy      241 SPPSPVIPPERPSAPLR 257
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Db      241 SRPSPVIPPERPSAPLR 257

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<!--EndFragment-->